

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 12:34:03 ; Search time 164 Seconds
(without alignments)
614.005 Million cell updates/sec

Title: US-10-618-281-11

Perfect score: 1277

Sequence: 1 SLHLSEADWQYSORELDAV.....ELYAQYLERLKFHELPHNS 241

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:

- 1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1277	100.0	241	5	US-10-618-281-11
2	1155.5	90.5	308	4	US-10-312-354-4
3	1110.5	87.0	338	4	US-10-087-192-315
4	1100.5	86.2	310	3	US-09-934-392-2
5	1100.5	86.2	310	4	US-10-398-037-65
6	1095.5	85.8	310	4	US-10-115-479-6
7	1069.5	83.8	285	5	US-10-618-281-16
8	1066.5	83.5	290	4	US-10-115-479-4
9	1065	83.4	458	4	US-10-363-616-280
10	1061	83.1	305	5	US-10-618-281-21
11	1037.5	81.2	236	5	US-10-618-281-39
12	1026.5	80.4	403	5	US-10-450-763-59338
13	954	74.7	286	6	US-11-097-143-24690
14	774	60.6	236	4	US-10-087-192-318
15	665	52.1	244	6	US-11-097-143-32013
16	616.5	48.3	364	5	US-10-739-930-10670
17	607.5	47.6	367	4	US-10-425-115-345880
18	603.5	47.3	305	4	US-10-425-115-296034
19	597	46.8	389	4	US-10-437-963-111752
20	594.5	46.6	383	4	US-10-425-115-201722
21	594.5	46.6	452	4	US-10-425-114-60109
22	593.5	46.5	546	4	US-10-437-963-185558
23	591.5	46.3	344	5	US-10-450-763-48788
24	581.5	45.5	395	4	US-10-437-963-150508
25	578.5	45.3	415	4	US-10-425-114-67729
26	578.5	45.3	415	4	US-10-425-115-213872
27	572.5	44.8	367	4	US-10-424-599-197073

28	565.5	44.3	301	4	US-10-437-963-125073	Sequence 125073,
29	561	43.9	234	3	US-09-934-392-6	Sequence 6, Appli
30	560.5	43.9	350	4	US-10-425-114-70216	Sequence 70216, A
31	559.5	43.8	347	5	US-10-481-032A-624	Sequence 624, App
32	559.5	43.8	384	4	US-10-437-963-139334	Sequence 139334,
33	551.5	43.2	353	4	US-10-424-599-201993	Sequence 201993,
34	548.5	43.0	296	4	US-10-425-115-224377	Sequence 224377,
35	538	42.1	390	5	US-10-481-032A-376	Sequence 376, App
36	532	41.7	375	4	US-10-425-115-213029	Sequence 213029,
37	515.5	40.4	104	3	US-09-925-299-939	Sequence 939, App
38	515.5	40.4	104	3	US-09-925-299-939	Sequence 939, App
39	515.5	40.4	104	3	US-10-106-698-5792	Sequence 5792, Ap
40	486	38.1	96	5	US-10-450-763-41797	Sequence 41797, A
41	484	37.9	217	4	US-10-408-765A-1081	Sequence 1081, Ap
42	478	37.4	339	4	US-10-424-599-143301	Sequence 143301,
43	443.5	34.7	260	5	US-10-450-763-48787	Sequence 48787, A
44	409	32.0	227	5	US-10-739-930-7680	Sequence 7680, Ap
45	405	31.7	186	4	US-10-425-115-232924	Sequence 232924,

ALIGNMENTS

RESULT 1
US-10-618-281-11
; Sequence 11, Application US/10618281
; Publication No. US20040219609A1
; GENERAL INFORMATION:
; APPLICANT: Day, Anthony G.
; APPLICANT: Estell, David A.
; APPLICANT: Lyons, Eric H.
; APPLICANT: Yao, Jian
; TITLE OF INVENTION: Methods for Modulating Proteins Not
; FILE REFERENCE: GC773-2
; CURRENT APPLICATION NUMBER: US/10/618,281
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 60/395,325
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-618-281-11

Query Match		100.0%;	Score 1277;	DB 5;	Length 241;
Best Local Similarity		100.0%;	Pred. No. 1.2e-128;		
Matches 241;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SLHLSEADWQYSORELDAV	FFSRTARDNRLGCMFVRCAPSSRYTL	FFSHGNAVDLGO	60
Db	1	SLHLSEADWQYSORELDAV	FFSRTARDNRLGCMFVRCAPSSRYTL	FFSHGNAVDLGO	60
Qy	61	MCSFVIGLSRINCNI	PSYDYSYGVSSGKPEKYLADIADA	WQALTRYGVSPENIL	120
Db	61	MCSFVIGLSRINCNI	PSYDYSYGVSSGKPEKYLADIADA	WQALTRYGVSPENIL	120
Qy	121	YGQSIGTVP	VDLASRYECAAVILHSLPMSGLRVAF	PDPTRKTYCFDAPPSDKISKVTSP	180
Db	121	YGQSIGTVP	VDLASRYECAAVILHSLPMSGLRVAF	PDPTRKTYCFDAPPSDKISKVTSP	180
Qy	181	VLVTHGTDEVID	FSHGLAMTERCPRAVEPLWVEGAGNDI	ELYAQYLERLKFHELPHN	240
Db	181	VLVTHGTDEVID	FSHGLAMTERCPRAVEPLWVEGAGNDI	ELYAQYLERLKFHELPHN	240
Qy	241	S	241		
Db	241	S	241		

RESULT 2

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OM protein - protein search, using sw model

Run on: November 21, 2005, 12:07:52 ; Search time 188 Seconds
(without alignments)
563.246 Million cell updates/sec

Title: US-10-618-281-11

Perfect score: 1277

Sequence: 1 SLHLSRADWQVSQRELDV.....ELYAQYLERLKQFIHELPS 241

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1277	100.0	241	8 ADU24063	Adu24063 Human ser
2	1266.5	99.2	242	8 ADN05213	Adn05213 Antipsori
3	1266.5	99.2	329	8 ADK71002	Adk71002 Human est
4	1259.5	98.6	322	8 ADS10621	Ads10621 Human the
5	1259.5	98.6	329	8 ADS10620	Ads10620 Human the
6	1252.5	98.1	247	7 ADF60194	Adf60194 Human con
7	1252.5	98.1	247	8 ADS11892	Ads11892 Human the
8	1252.5	98.1	247	8 ADS11891	Ads11891 Human the
9	1155.5	90.5	308	5 AAU81978	Aau81978 Human sec
10	1110.5	87.0	338	7 ABM85300	Abm85300 Mouse pro
11	1100.5	86.2	310	4 AAM93226	Aam93226 Human pol
12	1100.5	86.2	310	5 AAU77137	Aau77137 Human alp
13	1100.5	86.2	310	5 ABP43541	Abp43541 Human sec
14	1100.5	86.2	310	8 ADL30608	Adl30608 Human pro
15	1095.5	85.8	310	7 ADE15976	Ade15976 G-coupled
16	1095.5	85.8	310	8 ADL33915	Adl33915 Human G-c
17	1086	85.0	293	8 ADL27199	Adl27199 Amino aci
18	1069.5	83.8	285	8 ADU24068	Adu24068 Human ser
19	1066.5	83.5	290	7 ADE15974	Ade15974 G-coupled
20	1066.5	83.5	290	8 ADL33913	Adl33913 Human G-c
21	1066.5	83.5	310	8 ABM80127	Abm80127 Tumour-as
22	1065	83.4	361	8 ADO20182	Ado20182 Human PRO
23	1065	83.4	361	8 ABM81992	Abm81992 Tumour-as
24	1065	83.4	458	5 ABP62843	Abp62843 Human pol

25	1061	83.1	305	8 ADU24073	Adu24073 Human ser
26	1037.5	81.2	236	8 ADU24091	Adu24091 Human ser
27	1026.5	80.4	403	4 ABG27979	Abg27979 Novel hum
28	954	74.7	286	4 ABG65966	Abg65966 Drosophil
29	774	60.6	236	7 ABM85301	Abm85301 Human pro
30	769	60.2	236	9 ADY17790	Ady17790 PRO polyp
31	665	52.1	244	4 ABM868407	Abm868407 Drosophil
32	616.5	48.3	364	8 ADT60593	Adt60593 Plant pol
33	594.5	46.6	452	8 ADY04294	Ady04294 Plant ful
34	591.5	46.3	344	4 ABG18429	Abg18429 Novel hum
35	586.5	45.9	331	3 AAG20746	Aag20746 Arabidops
36	586.5	45.9	358	3 AAG20745	Aag20745 Arabidops
37	586.5	45.9	365	3 AAG20744	Aag20744 Arabidops
38	586.5	45.9	652	3 AAG51304	Aag51304 Arabidops
39	586.5	45.9	679	3 AAG51303	Aag51303 Arabidops
40	586.5	45.9	686	3 AAG51302	Aag51302 Arabidops
41	586	45.9	190	7 ADF58699	Adf58699 Human pol
42	578.5	45.3	415	8 ADY11914	Ady11914 Plant ful
43	572.5	44.8	361	8 ADN72995	Adn72995 Thale cre
44	572.5	44.8	361	8 ADN73587	Adn73587 Thale cre
45	571.5	44.8	335	3 AAG14422	Aag14422 Arabidops

ALIGNMENTS

RESULT 1
ADU24063
ID ADU24063 standard; protein; 241 AA.
XX
AC ADU24063;
XX
XX
DT 27-JAN-2005 (first entry)
XX
DE Human serine peptidase enzyme #3.
XX

Protease; cancer; immune-related disorder; cardiovascular disease;
brain-associated disease; neuronal-associated disease;
metabolic disorder; haematopoietic; cytostatic; immunosuppressive;
cardiovascular; cerebroprotective; neuroprotective; human;
serine peptidase; enzyme; peripheral nervous system; Alzheimer's disease;
Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis;
infection; ocular disease; migraine; pain; sexual dysfunction;
mood disorder; attention disorder; cognition disorder; hypotension;
hypertension; psychotic disorder; neurological disorder; dyskinesia;
organ transplant rejection.

XX Homo sapiens.
XX Key Location/Qualifiers
FT Domain 36..240
FT /note = Protease active domain
XX
XX US2004219609-A1.
XX 04-NOV-2004.
XX 11-JUL-2003; 2003US-00618281.
XX 12-JUL-2002; 2002US-0395325P.
XX (DAYA/) DAY A G.
XX (ESTE/) ESTELL D A.
XX (LYON/) LYONS E H.
XX (YAO/) YAO J.

XX Day AG, Estell DA, Lyons EH, Yao J;
XX WPI; 2004-794441/78.
XX Identifying compound that modulates activity of protease, by contacting
XX protease with test compound, measuring activity of protease before and
XX after contacting step, and determining whether test compound modulates

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OM protein - protein search, using sw model

Run on: November 21, 2005, 12:20:17 ; Search time 16 Seconds
(without alignments)
1449.265 Million cell updates/sec

Title: US-10-618-281-11

Perfect score: 1277

Sequence: 1 SLHLSERADWQYSQRELDV.....ELYAQYLERLKQFIHELPS 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	825.5	64.6	405	2 T23321	hypothetical prote
2	586.5	45.9	365	2 T05558	hypothetical prote
3	571.5	44.8	369	2 T48612	hypothetical prote
4	545.5	42.7	341	2 B8269	F21F23.4 protein -
5	534.5	41.9	422	2 D86446	hypothetical prote
6	525.5	41.2	316	2 C84635	hypothetical prote
7	481.5	37.7	256	2 G96692	hypothetical prote
8	462	36.2	307	2 C85363	hypothetical prote
9	399	31.2	245	2 AD2564	hypothetical prote
10	363.5	28.5	305	2 T20470	hypothetical prote
11	323.5	25.3	335	2 T20465	hypothetical prote
12	239.5	18.8	281	2 G70734	hypothetical prote
13	213.5	16.7	293	2 E65030	hypothetical prote
14	207.5	16.2	293	2 C85898	hypothetical prote
15	207.5	16.2	293	2 H91053	probable proteinase
16	202	15.8	284	2 S51294	probable enzyme li
17	189.5	14.8	292	2 AB0825	probable membrane
18	159.5	12.5	247	2 T17237	hypothetical prote
19	150	11.7	301	2 G83182	hypothetical prote
20	138	10.8	254	2 C95273	hypothetical prote
21	134.5	10.5	482	2 A44638	hypothetical prote
22	131.5	10.3	251	2 AF2674	hypothetical prote
23	131.5	10.3	4558	2 C82199	Atts protein limpo
24	122.5	9.6	261	2 T35708	RTX toxin RtxA Vc1
25	122	9.6	238	2 C69334	hydrolase - Strept
26	120.5	9.4	302	2 AB3196	2-hydroxy-6-oxonep
27	118.5	9.3	251	2 AD3177	arylester hydrolas
28	116	9.1	282	2 G75384	diptidyl peptida
29	116	9.1	318	2 T00552	probable lipase - lysophospholipase

30	114	8.9	330	2 D97235	probable hydrolase
31	112.5	8.8	340	2 T51482	lipase-like protei
32	111.5	8.7	283	2 B87546	acetoin dehydrogen
33	111.5	8.7	378	2 T41456	probable phosphol
34	110	8.6	305	2 F69966	hypothetical prote
35	109	8.5	320	2 F86821	hypothetical prote
36	108.5	8.5	289	2 S73722	triacylglycerol li
37	107.5	8.4	264	2 H75406	hydrolase, alpha/b
38	107.5	8.4	319	2 T47658	lipase-like protei
39	106.5	8.3	319	2 A11704	hypothetical prote
40	106.5	8.3	321	2 D83813	hypothetical prote
41	106.5	8.3	339	2 C83606	hypothetical prote
42	105.5	8.3	311	2 A86640	hypothetical prote
43	103.5	8.1	459	2 I60717	streptothricin-ace
44	102.5	8.0	471	2 T04911	hypothetical prote
45	102	8.0	304	2 T02661	lysophospholipase

ALIGNMENTS

RESULT 1

T23321
hypothetical protein K04G2.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change -09-Jul-2004
C:Accession: T23321
R:Gardner, A.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19727
A:Accession: T23321
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-405 <WIL>
A:Cross-references: UNIPROT:Q21221; UNIPARC:UPI000007F914; EMBL:Z75712; PIDN:CAB00039.1;
A:Experimental source: clone K04G2
C:Genetics:
A:Gene: CESP.K04G2.2
A:Map position: 1
A:introns: 2/2; 31/1; 104/2; 355/1

Query Match	64.6%	Score	825.5	DB	2	Length	405		
Best Local Similarity	66.1%	Pred. No.	5.4e-66						
Matches	152	Conservative	36	Mismatches	41	Indels	1	Gaps	1
Qy	7	RADWQYSQREL-DAVEVFSTRARDNRLGCMFVRCAPSSRYTLFLSHGNAVDLGQMSFY	65						
Db	146	RAANPHQEVDMANCVEMRITRRNRNVACTMIRPLPNSHFTLLFSGHNAVDLGQMTSFL	205						
Qy	66	IGLSRINCNI PSYDYGVSSEKPKSEKNLYADIDAAWQALTRYGVSPENILYQSI	125						
Db	206	YGLGFHLNCNVFSYDYGSGTSGKPKSEKNLYADITAAPELTKSBFGVPKEKILYQSI	265						
Qy	126	GTVPVTLASRYECAAVIDLHSLPLMSGLRVAFDPTRKTYCFDAFPISIDKISKVTVSPVLVTH	185						
Db	266	GTVPSVDLASHEDLAALVHLHPLMSGMRVAFPGITTTWCCDAFPSEIKVPRVKCPTLVTH	325						
Qy	186	GTEDEVIDFSHGLAMYRCRAVEPLWVEGAGHNDIELYAQYLERLKQFI	235						
Db	326	GTDEVIDFSHGVSIVRCPTSVPELWVPGAGHNDVHAAVLERLRSFI	375						

RESULT 2

T05558
hypothetical protein F22K18.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05558
R:Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mayer, K.F.
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15419
A:Accession: T05558
A:Molecule type: DNA

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OM protein - protein search, using sw model

Run on: November 21, 2005, 12:33:53 ; Search time 46 Seconds
(without alignments)
433.149 Million cell updates/sec

Title: US-10-618-281-11
Perfect score: 1277
Sequence: 1 SLHLSEADWQYSORELDAV.....ELVAYLERLQKFIHELPS 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RG_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943.5	73.9	374	2	US-09-270-767-45545
2	286	22.4	152	2	US-09-270-767-61054
3	227	17.8	263	2	US-09-902-540-12703
4	184.5	14.4	275	2	US-09-248-796A-15244
5	150	11.7	661	2	US-09-252-991A-18225
6	149.5	11.7	312	2	US-09-107-532A-5684
7	126.5	9.9	2807	2	US-09-543-681A-4980
8	118.5	9.3	339	2	US-09-489-847-350
9	118.5	9.3	554	2	US-09-489-847-352
10	117.5	9.2	398	2	US-09-107-532A-6418
11	110	8.6	305	2	US-09-462-845-9
12	110	8.6	305	2	US-10-402-312-9
13	110	8.6	305	2	US-10-401-437-9
14	110	8.6	305	2	US-10-402-067-9
15	110	8.6	305	2	US-10-401-436-9
16	109.5	8.6	271	2	US-09-710-279-2822
17	109.5	8.6	271	2	US-09-710-279-3308
18	109.5	8.6	284	2	US-09-134-001C-2927
19	107	8.4	300	2	US-09-355-166-4
20	106.5	8.3	374	2	US-09-252-991A-27773
21	106	8.3	296	2	US-09-902-540-10861
22	100	7.8	346	1	US-08-602-359A-34
23	99.5	7.8	255	2	US-09-489-039A-9075
24	98.5	7.7	297	1	US-08-602-359A-37
25	95	7.4	298	2	US-09-902-540-10513
26	93.5	7.3	310	2	US-09-328-352-7313
27	93.5	7.3	589	2	US-09-252-991A-31105

28	93	7.3	210	2	US-09-902-540-11094	Sequence 11094, A
29	91	7.1	278	2	US-09-522-401-2	Sequence 2, Appli
30	89	7.0	342	2	US-09-489-039A-8276	Sequence 8276, Ap
31	89	7.0	285	2	US-09-328-352-7483	Sequence 7483, Ap
32	89	7.0	293	2	US-09-328-352-6002	Sequence 6002, Ap
33	88.5	6.9	651	2	US-09-902-540-11752	Sequence 11752, A
34	88	6.9	841	2	US-09-518-550-44	Sequence 44, Appl
35	87.5	6.9	369	2	US-09-198-452A-1001	Sequence 1001, Ap
36	87.5	6.9	372	2	US-09-438-185A-931	Sequence 931, App
37	87	6.8	261	2	US-09-902-540-13754	Sequence 13754, A
38	86	6.7	248	2	US-08-935-263-14	Sequence 14, Appl
39	86	6.7	248	2	US-09-594-185-14	Sequence 14, Appl
40	86	6.7	248	2	US-10-033-078-14	Sequence 14, Appl
41	86	6.7	248	2	US-10-763-933-14	Sequence 14, Appl
42	86	6.7	258	2	US-09-252-991A-20260	Sequence 20260, A
43	86	6.7	277	2	US-09-424-349A-6	Sequence 6, Appli
44	86	6.7	334	2	US-09-902-540-11426	Sequence 11426, A
45	85.5	6.7	319	2	US-09-328-352-5110	Sequence 5110, Ap

ALIGNMENTS

RESULT 1
US-09-270-767-45545
; Sequence 45545, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45545
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45545

Query Match		73.9%	Score 943.5;	DB 2;	Length 374;
Best Local Similarity		72.0%	Pred. No. 2.4e-97;		
Matches 170;		Conservative 37;	Mismatches 28;	Indels 1;	Gaps 1;
QY	1	SLHLSEADWQYSORELDAVEVFFSRTARDNRLGCMFVRCAPSSRYTLFLFSGNAVDLGO	60		
DB	54	NLQLFDRAEWQYSEREKSKVEAFFRTSRGNLITCIYVRCNKAKYTLFLFSGNAVDLGO	113		
QY	61	MCSFYIGLSRINCNIIFYSYGVSGKPKSEKNLYADIDAQAL-RTRYGVSPENII	119		
DB	114	MSSFYTLGSQLNCINIFGYDSYGVSGKPKSEKNLYADIEAAQAMXRTFNISPETII	173		
QY	120	LYGQSIGVPTVDLASRYECARVILHSLPLMSGLRVAFDPDTRKTYCPDAPSDKISKVYS	179		
DB	174	LYGQSIGVPTVDLASRHEVGAVILHSLPLMSGLRVVFRNTKRTWTFDAPSDKIAKVA	233		
QY	180	PVLVIHGTEDEVIDFSHGLAMYERCPRAVEPLWVGAGHNDIELVAYLERLQKFI	235		
DB	234	PVLVIHGTDDEVIDFSHGIYERCPKTVPEPPWVGAGHNDVELHPHYERLQKFL	289		

RESULT 2
US-09-270-767-61054
; Sequence 61054, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767

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OM protein - protein search, using sw model

Run on: November 21, 2005, 12:37:13 ; Search time 6 seconds
(without alignments)
45.380 Million cell updates/sec

Title: US-10-618-281-11

Perfect score: 1277

Sequence: 1 SLHBRADWQYSQRELDV.....ELYAQYLERLKQFIHELPSN 241

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA New:
- 1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	107	8.4	300	7	US-11-179-977-4
2	78	6.1	256	7	US-11-179-977-2
3	74	5.8	872	7	US-11-077-550-145
4	69.5	5.4	319	7	US-11-109-156-38
5	69.5	5.4	323	7	US-11-109-156-37
6	68.5	5.4	242	7	US-11-179-977-14
7	65.5	5.1	330	1	US-10-689-742-82
8	65.5	5.1	657	7	US-11-179-977-1
9	64	5.0	289	7	US-11-179-977-11
10	63.5	5.0	325	7	US-11-074-176-370
11	63.5	5.0	429	7	US-11-074-176-248
12	63	4.9	521	7	US-11-109-156-34
13	60	4.7	298	7	US-11-179-977-6
14	59.5	4.7	520	7	US-11-098-662-12
15	59.5	4.7	799	7	US-11-074-176-348
16	59.5	4.7	805	7	US-11-074-176-172
17	59	4.6	119	1	US-10-502-145-25
18	59	4.6	256	7	US-11-179-977-15
19	59	4.6	318	7	US-11-179-977-16
20	58.5	4.6	211	7	US-11-098-662-16
21	58.5	4.6	2376	7	US-11-096-051-4
22	58.5	4.6	2715	7	US-11-096-051-2
23	58	4.5	2280	7	US-11-022-562-211
24	57.5	4.5	876	7	US-11-077-550-82
25	57.5	4.5	1332	7	US-11-091-643-18

26	57.5	4.5	2721	7	US-11-096-051-10	Sequence 10, Appl
27	57.5	4.5	2725	7	US-11-096-051-8	Sequence 8, Appli
28	57	4.5	390	7	US-11-082-389-42	Sequence 42, Appl
29	57	4.5	390	7	US-11-082-389-44	Sequence 44, Appl
30	57	4.5	569	1	US-10-632-150-2	Sequence 2, Appli
31	57	4.5	902	7	US-11-057-058-64	Sequence 64, Appl
32	56.5	4.4	863	7	US-11-077-550-36	Sequence 36, Appl
33	56.5	4.4	876	7	US-11-077-550-106	Sequence 106, App
34	56.5	4.4	876	7	US-11-077-550-108	Sequence 108, App
35	56.5	4.4	910	1	US-10-131-826A-112	Sequence 112, App
36	56.5	4.4	932	7	US-11-017-550-65	Sequence 65, Appl
37	56.5	4.4	1127	7	US-11-077-550-54	Sequence 54, Appl
38	56.5	4.4	1129	7	US-11-077-550-52	Sequence 52, Appl
39	56	4.4	174	1	US-10-984-376-7	Sequence 7, Appli
40	56	4.4	467	7	US-11-082-389-334	Sequence 334, App
41	56	4.4	475	1	US-10-510-386-98	Sequence 98, Appl
42	56	4.4	552	1	US-10-131-826A-196	Sequence 196, App
43	55.5	4.3	406	1	US-10-131-826A-66	Sequence 66, Appl
44	55.5	4.3	406	1	US-10-131-826A-258	Sequence 258, App
45	55.5	4.3	487	1	US-10-131-826A-528	Sequence 528, App

ALIGNMENTS

RESULT 1
US-11-179-977-4
; Sequence 4, Application US/11179977
; Publication No. US20050249789A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
; FILE REFERENCE: GC511-PCT
; CURRENT APPLICATION NUMBER: US/11/179,977
; CURRENT FILING DATE: 2005-07-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Bacillus
US-11-179-977-4

Query Match 8.4%; Score 107; DB 7; Length 300;
Best Local Similarity 21.7%; Pred. No. 2.9e-05;
Matches 49; Conservative 41; Mismatches 94; Indels 42; Gaps 11;

Qy	47	TLFSGH---	NAVDLQMC	SVFYIGLS	RINCNI	FSYDYG	VGSGKPKSEK	NLYA--	DID	101			
Db	83	TLIICHG	VTMNV	LSIKYMH	LFDLG---	WNVL	YDHRH	RGSGKTSYGF	YKDDL	138			
Qy	102	AAWQAL	TRTYG	SPENII	-LYQSGISG	TGTVPTV	-----	DLASRY	--ECAA	VILH	150		
Db	139	KVVSLL	KNK--	-TNH	RGLIGH	GSCMG	AVTALL	YAGAH	CSGD	GADFY	ADCP	196	
Qy	151	GLRVA-----	FPDTR	KTYCF	DAPSID	KISKVTS	PLVH	CTE	VIDF	FSH	196		
Db	197	RLRAEY	RLPSW	PLP	LPAD	FFLKL	RGYRA	REVS	PLAVID	KIEK	PVLF	256	
Qy	197	GLAMY	ERC	PR	AVE	PLM	VEG	AGH	NDIEL	YAO---	YLER	LKQFI	238
Db	257	TERLYE	K-KG	P	KAL	Y	AE	NGE	HAMS	-YTK	NRYTR	KTV	300

RESULT 2
US-11-179-977-2
; Sequence 2, Application US/11179977
; Publication No. US20050249789A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
; FILE REFERENCE: GC511-PCT
; CURRENT APPLICATION NUMBER: US/11/179,977